



2 1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/613,508B
DATE: 07/10/2003
TIME: 15:35:50

Input Set : A:\PF140P1D1 PatentIn - FINAL and CORRECT.ST25.txt
Output Set: N:\CRF4\07102003\I613508B.raw

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3 <110> APPLICANT: He, et al.
5 <120> TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease
6 and 4
8 <130> FILE REFERENCE: PF140P1D1
10 <140> CURRENT APPLICATION NUMBER: 09/613,508B
11 <141> CURRENT FILING DATE: 2000-07-10
13 <150> PRIOR APPLICATION NUMBER: 08/462,969
14 <151> PRIOR FILING DATE: 1995-06-05
16 <150> PRIOR APPLICATION NUMBER: 08/334,251
17 <151> PRIOR FILING DATE: 1994-11-01
19 <160> NUMBER OF SEQ ID NOS: 14
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1369
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <400> SEQUENCE: 1
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33 gcggggacac gggctcgctt gggctcttcc acccctgcgg agcgcactac cccgagccag 180
35 gggcggtgca agccccgccc ggccctaccc agggcggtc ctccctccgc agcgccgaga 240
37 ctttttagttt cgctttcgct aaaggggccc cagacccttg ctgcggagcg acggagagag 300
39 actgtgccag tcccagccgc cctaccgccc tgggaacgat ggcagatgat cagggctgta 360
41 ttgaagagca ggggggttag gattcagcaa atgaagattc agtggatgct aagccagacc 420
43 ggtcctcggt tgtaccgtcc ctcttcagta agaagaagaa aaatgtcacc atgcatcca 480
45 tcaagaccac ccgggaccga gtgcctacat atcagtacaa catgaatttt gaaaagctgg 540
47 gcaaatgcat cataataaac aacaagaact ttgataaagt gacaggtagt ggcgttcgaa 600
49 acggaacaga caaagatgcc gaggcgtct tcaagtgtt ccgaagcctg ggttttgacg 660
51 tgattgtcta taatgactgc tcttggtgca agatgcaaga tctgcttaaa aaagcttctg 720
53 aagaggacca tacaatgcc gctgcttcg cctgcctcct ctttaagccat ggagaagaaa 780
55 atgtaattta tgggaaagat ggtgtcacac caataaagga tttgacagcc cactttaggg 840
57 gggatagatg caaaaccctt ttagagaaac ccaaactctt cttcattcag gcttgccgag 900
59 ggaccgagct tgatgatgcc atocaggccg actcggggcc catcaatgac acagatgcta 960
61 atcctcgata caagatccca gtggaagctg acttctctt cgcctattcc acggttccag 1020
63 gctattactc gtggaggagc ccaggaagag gctcctggtt tgtgcaagcc ctctgctcca 1080
65 tcttgaggga gcacggaaaa gacctggaaa tcatgcagat cctcaccagg gtgaatgaca 1140
67 gagttgccag gcactttgag tctcagtcgt atgaccaca cttccatgag aagaagcaga 1200
69 tcccctgtgt ggtctccatg ctaccaagg aactctactt cagtcaatag ccatatcagg 1260
71 ggtacattct agctgagaag caatgggtca ctcattaatg aatcacattt ttttatgctc 1320
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76 <210> SEQ ID NO: 2
77 <211> LENGTH: 303
78 <212> TYPE: PRT

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79 <213> ORGANISM: Homo sapiens

81 <400> SEQUENCE: 2

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88          20          25          30
91 Pro Ser Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile
92          35          40          45
95 Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe
96          50          55          60
99 Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys
100 65          70          75          80
103 Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala
104          85          90          95
107 Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn
108          100          105          110
111 Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu
112          115          120          125
115 Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His
116          130          135          140
119 Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys
120 145          150          155          160
123 Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu
124          165          170          175
127 Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp
128          180          185          190
131 Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn
132          195          200          205
135 Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser
136          210          215          220
139 Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp
140 225          230          235          240
143 Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu
144          245          250          255
147 Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His
148          260          265          270
151 Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile
152          275          280          285
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159 <210> SEQ ID NO: 3

160 <211> LENGTH: 1159

161 <212> TYPE: DNA

162 <213> ORGANISM: Homo sapiens

164 <400> SEQUENCE: 3

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169 gccgtgagga gttagcgagc cctgctcaca ctggcgctc tggttttcgg tgggtgtgcc      180
171 ctgcacctgc ctcttccgcg attctcatta ataaaggtat ccatggagaa cactgaaaac      240

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173 tcagtggatt caaaatccat taaaaatttg gaaccaaaga tcatacatgg aagcgaatca 300
175 atggactctg gaatatccct ggacaacagt tataaaatgg attatcctga gatgggttta 360
177 tgtataataa ttaataataa gaattttcat aaaagcactg gaatgacatc tcggtctggt 420
179 acagatgtcg atgcagcaaa cctcagggaa acattcagaa acttgaaata tgaagtcagg 480
181 aataaaaaatg atcttacacg tgaagaaatt gtggaattga tgcgtgatgt ttctaaagaa 540
183 gatcacagca aaaggagcag ttttgtttgt gtgcttctga gccatggtga agaaggaata 600
185 atttttggaa caaatggacc tgttgacctg aaaaaataa caaacttttt cagaggggat 660
187 cgttgtagaa gtctaactgg aaaacccaaa cttttcatta ttcaggcctg ccgtggtaca 720
189 gaactggact gtggcattga gacagacagt ggtgttgatg atgacatggc gtgtcataaa 780
191 ataccagtgg aggccgactt cttgtatgca tactccacag cacctggtta ttattcttgg 840
193 cgaaattcaa aggatggctc ctggttcacg cagtcgcttt gtgccatgct gaaacagtat 900
195 gccgacaagc ttgaatttat gcacattctt acccgggtta accgaaagggt ggcaacagaa 960
197 tttgagtcct tttcctttga cgctactttt catgcaaaga aacagattcc atgtattggt 1020
199 tccatgctca caaaagaact ctatttttat cactaaagaa atggttgggt ggtggttttt 1080
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206 <210> SEQ ID NO: 4
207 <211> LENGTH: 277
208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 4
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217 Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
218 20 25 30
221 Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
222 35 40 45
225 Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
226 50 55 60
229 Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
230 65 70 75 80
233 Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
234 85 90 95
237 Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
238 100 105 110
241 Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
242 115 120 125
245 Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
246 130 135 140
249 Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
250 145 150 155 160
253 Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
254 165 170 175
257 Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
258 180 185 190
261 Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
262 195 200 205
265 Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
266 210 215 220

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269 Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
 270 225 230 235 240
 273 Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
 274 245 250 255
 277 His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
 278 260 265 270

281 Leu Tyr Phe Tyr His

282 275

285 <210> SEQ ID NO: 5

286 <211> LENGTH: 31

287 <212> TYPE: DNA

288 <213> ORGANISM: Artificial sequence

290 <220> FEATURE:

291 <223> OTHER INFORMATION: Contains a Bam HI restriction enzyme site (underlined)
 followed

292 by 18 nucleotides of ICE-LAP-3 coding sequence starting from the

293 presumed terminal amino acid of the processed protein codon

295 <400> SEQUENCE: 5

296 gatcggatcc atgcgtgcgg ggacacgggt c 31

299 <210> SEQ ID NO: 6

300 <211> LENGTH: 31

301 <212> TYPE: DNA

302 <213> ORGANISM: Artificial sequence

304 <220> FEATURE:

305 <223> OTHER INFORMATION: Contains complementary sequences to an Xba I site followed
 by 21

306 nucleotides of ICE-LAP-3

308 <400> SEQUENCE: 6

309 gtactctaga tcattcaccc tgggtggagga t 31

312 <210> SEQ ID NO: 7

313 <211> LENGTH: 31

314 <212> TYPE: DNA

315 <213> ORGANISM: Artificial sequence

317 <220> FEATURE:

318 <223> OTHER INFORMATION: Contains a Bam HI restriction enzyme site followed by 18

319 nucleotides of ICE-LAP-4 coding sequence starting from the

320 presumed terminal amino acid of the processed protein codon

322 <400> SEQUENCE: 7

323 gatcggatcc atggagaaca ctgaaaactc a 31

326 <210> SEQ ID NO: 8

327 <211> LENGTH: 31

328 <212> TYPE: DNA

329 <213> ORGANISM: Artificial sequence

331 <220> FEATURE:

332 <223> OTHER INFORMATION: Contains complementary sequences to an Xba I site followed
 by 21

333 nucleotides of ICE-LAP-4

335 <400> SEQUENCE: 8

336 gtactctaga ttagtgataa aaatagagtt c 31

339 <210> SEQ ID NO: 9

340 <211> LENGTH: 22

341 <212> TYPE: DNA

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342 <213> ORGANISM: Artificial sequence

344 <220> FEATURE:

345 <223> OTHER INFORMATION: Contains the ICE-LAP-3 translational initiation site ATG followed

346 by 5 nucleotides of ICE-LAP-3 coding sequence starting from the

347 initiation codon

349 <400> SEQUENCE: 9

350 gactatgcgt gcggggacac gg 22

353 <210> SEQ ID NO: 10

354 <211> LENGTH: 53

355 <212> TYPE: DNA

356 <213> ORGANISM: Artificial sequence

358 <220> FEATURE:

359 <223> OTHER INFORMATION: Contains translation stop codon, HA tag and the last 21

360 nucleotides of the ICE-LAP-3 coding sequence, not including the

361 stop codon

363 <400> SEQUENCE: 10

364 aatcaagcgt agtctgggac gtcgtatggg tattcaccct ggtggaggat ttg 53

367 <210> SEQ ID NO: 11

368 <211> LENGTH: 21

369 <212> TYPE: DNA

370 <213> ORGANISM: Artificial sequence

372 <220> FEATURE:

373 <223> OTHER INFORMATION: Contains the ICE-LAP-4 translational initiation site, ATG,

374 followed by 15 nucleotides of ICE-LAP-4 coding sequence starting

375 from the initiation codon

377 <400> SEQUENCE: 11

378 accatggaga acactgaaaa c 21

381 <210> SEQ ID NO: 12

382 <211> LENGTH: 53

383 <212> TYPE: DNA

384 <213> ORGANISM: Artificial sequence

386 <220> FEATURE:

387 <223> OTHER INFORMATION: Contains translation stop codon, HA tag and the last 21

388 nucleotides of the ICE-LAP-4 coding sequence, not including the

389 stop codon

391 <400> SEQUENCE: 12

392 aatcaagcgt agtctgggac gtcgtatggg tagtgataaa aatagagttc ttt 53

395 <210> SEQ ID NO: 13

396 <211> LENGTH: 503

397 <212> TYPE: PRT

398 <213> ORGANISM: Caenorhabditis elegans

400 <400> SEQUENCE: 13

402 Met Met Arg Gln Asp Arg Arg Ser Leu Leu Glu Arg Asn Ile Met Met

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406 Phe Ser Ser His Leu Lys Val Asp Glu Ile Leu Glu Val Leu Ile Ala

407 20 25 30

410 Lys Gln Val Leu Asn Ser Asp Asn Gly Asp Met Ile Asn Ser Cys Gly

411 35 40 45

414 Thr Val Arg Glu Lys Arg Arg Glu Ile Val Lys Ala Val Gln Arg Arg

VERIFICATION SUMMARY

DATE: 07/10/2003

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